Title: Multiple sequence alignment using genetic algorithms
Author: Zdeněk Pátek
Department: Department of Software and Computer Science Education
Supervisor: RNDr. František Mráz, CSc.

Abstract:
The thesis adresses the problem of multiple sequence alignment (MSA). It contains the specication of the proposed method MSAMS that allows to find motifs in biological sequences, to split sequences to blocks using the motifs, to solve MSA on the blocks and nally to assemble the global alignment from the aligned blocks and motifs. Motif search and MSA are both solved using genetic algorithms. The thesis describes the implementation of the method, conguration of its settings, benchmarking on the BAliBASE database and comparison to the ClustalW program. Experimental results showed that MSAMS can discover better alignments than ClustalW.

Keywords: multiple sequence alignment, motif nding, genetic algorithms, ClustalW